

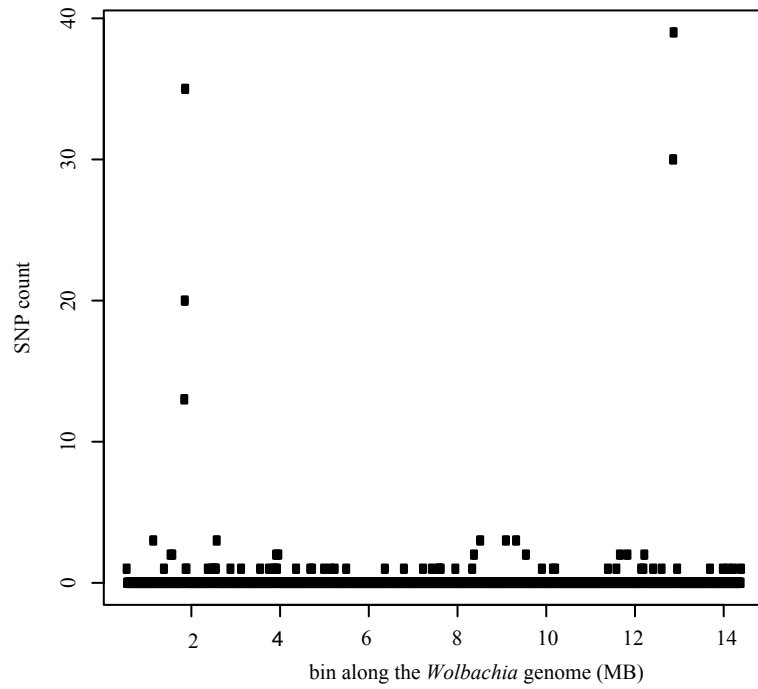
## Supplementary Information

Population genomics of *Wolbachia* and mtDNA in *Drosophila simulans* from California

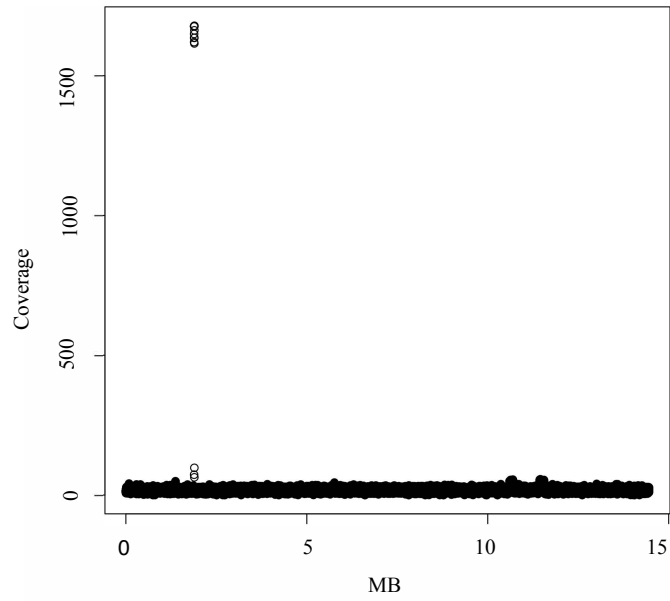
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Key words: *Drosophila simulans*, population genetics, *Wolbachia*



Supplementary Figure 1: SNP density in the *Wolbachia* genome. Two regions were excluded from the final set of SNPs due to unusual SNP density, shown here. These regions also coincided with regions of unusually high coverage, suggesting they are repetitive.



Supplementary Figure 2: An example of coverage across the *Wolbachia* genome, with a large outlier that was excluded from the final analysis. This region corresponds to one of the regions of unusually high SNP density, shown in Supp. Figure 1.

| CHR   | SNP      | <i>p</i> -value |
|-------|----------|-----------------|
| 2R    | 5814103  | 1.47E-06        |
| 2R    | 5811053  | 3.37E-06        |
| 2R    | 13567097 | 5.61E-06        |
| 2R    | 13550916 | 6.41E-06        |
| 2R    | 13566886 | 6.72E-06        |
| 2R    | 13566065 | 6.87E-06        |
| 2R    | 13555805 | 7.01E-06        |
| 2R    | 13567885 | 7.06E-06        |
| 2R    | 13569038 | 7.27E-06        |
| 2R    | 13553992 | 7.29E-06        |
| 2R    | 13564712 | 7.29E-06        |
| 2R    | 13565153 | 7.42E-06        |
| 2R    | 13566442 | 7.65E-06        |
| 2R    | 13568212 | 7.70E-06        |
| 2R    | 13558515 | 7.97E-06        |
| 3L    | 2055556  | 8.24E-06        |
| mtDNA | 12354    | 3.18E-06        |

Supplementary Table 1: The full results of the association analysis. Note that while all significant results are included, 2R and 3L are the results of a multivariate analysis of *Wolbachia* and mtDNA titre while the significant hit for mtDNA was the result of a *Wolbachia* titre alone.